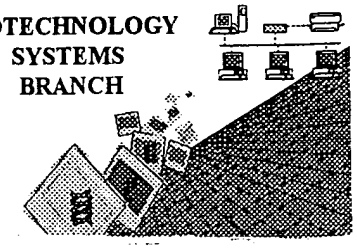
CSP
1007

BIOTECHNOLOGY
SYSTEMS
BRANCH



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/[illegible]26,106C
Source: CIPE
Date Processed by STIC: 10/8/02

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO **REDUCE** ERRORED SEQUENCE LISTINGS, **PLEASE** USE THE **CHECKER VERSION 3.1 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
http://www.uspto.gov/web/offices/pac/checker

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<**http://www.uspto.gov/ebc/efs/downloads/documents.htm**> , **EFS Submission User Manual** - ePAVE)
2. **U.S. Postal Service:** U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
3. **Hand Carry directly to:**
   U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202
   Or
   U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. **Federal Express, United Parcel Service, or other delivery service to:** U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 01/29/2002

OIPE

Raw Sequence Listing Error Summary

ERROR DETECTED | **SUGGESTED CORRECTION** | SERIAL NUMBER: 10/026,106C

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 ✓ Wrapped Nucleics Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
2 ____ Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.
3 ✓ Misaligned Amino Numbering	The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
4 ____ Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
5 ____ Variable Length	Sequence(s)____contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
6 ____ PatentIn 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
7 ____ Skipped Sequences (OLD RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
8 ____ Skipped Sequences (NEW RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence. <210> sequence id number <400> sequence id number 000
9 ____ Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
10 ____ Invalid <213> Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
11 ____ Use of <220>	Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
12 ____ PatentIn 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
13 ____ Misuse of n	n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

OIPE

Does Not Comply
Corrected Diskette Needed

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/026,106C

DATE: 10/08/2002
TIME: 13:59:24

Input Set : A:\EP.txt
Output Set: N:\CRF4\10082002\J026106C.raw

```
     1 <110> APPLICANT: Renauld, Jean-Christophe
     2       Fickensicher, Helmut
     3       Dumoutier, Laure
     4       Hor, Simon
     6 <120> TITLE OF INVENTION: Isolated Cytokine Receptor LICR-2
     8 <130> FILE REFERENCE: LUD 5752 NDH
C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/026,106C
    12 <141> CURRENT FILING DATE: 2001-12-21
    14 <160> NUMBER OF SEQ ID NOS: 19
```

ERRORED SEQUENCES

Amino numbering misaligned.
See error summary sheet item 3

```
    104 <210> SEQ ID NO: 8
    105 <211> LENGTH: 522
    106 <212> TYPE: PRT
    107 <213> ORGANISM: Homo sapiens
W--> 108 <220> FEATURE:
W--> 109 <400> SEQUENCE: 8
    110 Met Ala Gly Pro Glu Arg Trp Gly Pro Leu Leu Leu Cys Leu Leu Gln
    111 1               5                  10                  15
    112 Ala Ala Pro Gly Arg Pro Arg Leu Ala Pro Pro Gln Asn Val Thr Leu
    113             20                  25                  30
    114 Leu Ser Gln Asn Phe Ser Val Tyr Leu Thr Trp Leu Pro Gly Leu Gly
    115         35                  40                  45
    116 Asn Pro Gln Asp Val Thr Tyr Phe Val Ala Tyr Gln Ser Ser Pro Thr
    117     50                  55                  60
    118 Arg Arg Arg Trp Arg Glu Val Glu Glu Cys Ala Gly Thr Lys Glu Leu
    119 65                  70                  75                  80
    120   Leu Cys Ser Met Met Cys Leu Lys Lys Gln Asp Leu Tyr Asn Lys Phe
E--> 121                 85                  90                  95
    122 Lys Gly Arg Val Arg Thr Val Ser Pro Ser Ser Lys Ser Pro Trp Val
E--> 123             100                 105                 110
    124 Glu Ser Glu Tyr Leu Asp Tyr Leu Phe Glu Val Glu Pro Ala Pro Pro
E--> 125         115                 120                 125
    126 Val Leu Val Leu Thr Gln Thr Glu Glu Ile Leu Ser Ala Asn Ala Thr
E--> 127     130                 135                 140
    128 Tyr Gln Leu Pro Pro Cys Met Pro Pro Leu Asp Leu Lys Tyr Glu Val
E--> 129 145                 150                 155                 160
    130 Ala Phe Trp Lys Glu Gly Ala Gly Asn Lys Thr Leu Phe Pro Val Thr
E--> 131                 165                 170                 175
    132 Pro His Val Thr Pro His Gly Gln Pro Val Gln Ile Thr Leu Gln Pro
E--> 133             180                 185                 190
```

RAW SEQUENCE LISTING DATE: 10/08/2002
PATENT APPLICATION: US/10/026,106C TIME: 13:59:24

Input Set : A:\EP.txt
Output Set: N:\CRF4\10082002\J026106C.raw

```
     134 Ala Ala Ser Glu His His Cys Leu Ser Ala Arg Thr Ile Tyr Thr Phe
E--> 135         195                 200                 205
     136 Ser Val Pro  Lys Tyr Ser Lys Phe Ser Lys Pro Thr Cys Phe Leu Leu
E--> 137     210                 215                 220
     138 Glu Val Pro Glu Ala Asn Trp Ala Phe Leu Val Leu Pro Ser Leu Leu
E--> 139 225                 230                 235                 240
     141 Ile Leu Leu Leu Val Ile Ala Ala Gly Gly Val Ile Trp Lys Thr Leu
E--> 142                 245                 250                 255
     143 Met Gly Asn Pro Trp Phe Gln Arg Ala Lys Met Pro Arg Ala Leu Asp
E--> 144             260                 265                 270
     145 Phe Ser Gly His Thr Thr His Pro Val Ala Thr Phe Gln Pro Ser Arg
E--> 146         275                 280                 285
     147 Pro Glu Ser Val Asn Asp Leu Phe Leu Cys Pro Gln Lys Glu Leu Thr
E--> 148     290                 295                 300
     149 Arg Gly Val Arg Pro Thr Pro Arg Val Arg Pro Ala Thr Gln Gln Thr
E--> 150 305                 310                 315                 320
     153 Arg Trp Lys Lys Asp Leu Ala Glu Asp Glu Glu Glu Glu Asp Thr Glu
E--> 154                 325                 330                 335
     155 Asp Gly Val Ser Phe Gln Pro Tyr Ile Glu Pro Pro Ser Phe Leu Gly
E--> 156             340                 345                 350
     157 Gln Glu His Gln Ala Pro Gly His Ser Glu Ala Gly Gly Val Asp Ser
E--> 158         355                 360                 365
     159 Gly Arg Pro Arg Ala Pro Leu Val Pro Ser Glu Gly Ser Ser Ala Trp
E--> 160     370                 375                 380
     161 Asp Ser Ser Asp Arg Ser Trp Ala Ser Thr Val Asp Ser Ser Trp Asp
E--> 162 385                 390                 395                 400
     163 Arg Ala Gly Ser Ser Gly Tyr Leu Ala Glu Lys Gly Pro Gly Gln Gly
E--> 164                 405                 410                 415
     165 Pro Gly Gly Asp Gly His Gln Glu Ser Leu Pro Pro Pro Glu Phe Ser
E--> 166             420                 425                 430
     167 Lys Asp Ser Gly Phe Leu Glu Glu Leu Pro Glu Asp Asn Leu Ser Ser
E--> 168         435                 440                 445
     169 Trp Ala Thr Trp Gly Thr Leu Pro Pro Glu Pro Pro Asn Leu Val Pro
E--> 170     450                 455                 460
     172 Gly Gly Pro Pro Val Ser Leu Gln Thr Leu Thr Phe Cys Trp Glu Ser
E--> 173 465                 470                 475                 480
     174 Ser Pro Glu Glu Glu Glu Glu Ala Arg Glu Ser Glu Ile Glu Asp Ser
E--> 175                 485                 490                 495
     176 Asp Ala Gly Ser Trp Gly Ala Glu Ser Thr Gln Arg Thr Glu Asp Arg
E--> 177             500                 505                 510
     178 Gly Arg Thr Leu Gly His Tyr Met Ala Arg        515
E--> 179   520
     220 <210> SEQ ID NO: 10
     221 <211> LENGTH: 244
     222 <212> TYPE: PRT
     223 <213> ORGANISM: Homo sapiens
W--> 224 <220> FEATURE:
W--> 225 <400> SEQUENCE: 10
     227 Met Ala Gly Pro Glu Arg Trp Gly Pro Leu Leu Leu Cys Leu Leu Gln
```

RAW SEQUENCE LISTING DATE: 10/08/2002
PATENT APPLICATION: US/10/026,106C TIME: 13:59:24

Input Set : A:\EP.txt
Output Set: N:\CRF4\10082002\J026106C.raw

```
228 1                5                  10                  15
229 Ala Ala Pro Gly Arg Pro Arg Leu Ala Pro Pro Gln Asn Val Thr Leu
230              20                  25                  30
231 Leu Ser Gln Asn Phe Ser Val Tyr Leu Thr Trp Leu Pro Gly Leu Gly
232          35                  40                  45
233 Asn Pro Gln Asp Val Thr Tyr Phe Val Ala Tyr Gln Ser Ser Pro Thr
234      50                  55                  60
235 Arg Arg Arg Trp Arg Glu Val Glu Glu Cys Ala Gly Thr Lys Glu Leu
236 65                  70                  75                  80
237   Leu Cys Ser Met Met Cys Leu Lys Lys Gln Asp Leu Tyr Asn Lys Phe
E--> 238                85                  90                  95
239 Lys Gly Arg Val Arg Thr Val Ser Pro Ser Ser Lys Ser Pro Trp Val
E--> 240             100                 105                 110
241 Glu Ser Glu Tyr Leu Asp Tyr Leu Phe Glu Val Glu Pro Ala Pro Pro
E--> 242         115                 120                 125
243 Val Leu Val Leu Thr Gln Thr Glu Glu Ile Leu Ser Ala Asn Ala Thr
E--> 244     130                 135                 140
245 Tyr Gln Leu Pro Pro Cys Met Pro Pro Leu Asp Leu Lys Tyr Glu Val
E--> 246 145                 150                 155                 160
247 Ala Phe Trp Lys Glu Gly Ala Gly Asn Lys Thr Leu Phe Pro Val Thr
E--> 248                165                 170                 175
249 Pro His Gly Gln Pro Val Gln Ile Thr Leu Gln Pro Ala Ala Ser Glu
E--> 250             180                 185                 190
251 His His Cys Leu Ser Ala Arg Thr Ile Tyr Thr Phe Ser Val Pro Lys
E--> 252         195                 200                 205
253 Tyr Ser Lys Phe Ser Lys Pro Thr Cys Phe Leu Leu Glu Val Pro Gly
E--> 256     210                 215                 220
257 Leu Phe Trp Thr His Thr Pro Cys Gly Asn Leu Ser Ala Gln Gln Thr
E--> 258 225                 230                 235                 240
259 Arg Val Arg Glu
294 <210> SEQ ID NO: 15
295 <211> LENGTH: 27
296 <212> TYPE: DNA
297 <213> ORGANISM: Homo sapiens
W--> 298 <220> FEATURE:
W--> 299 <400> SEQUENCE: 15
E--> 300 aatgtctaga tgctgttctc atttacc
301 (27)
313 <210> SEQ ID NO: 17
314 <211> LENGTH: 20
315 <212> TYPE: DNA
316 <213> ORGANISM: Homo sapiens
W--> 317 <220> FEATURE:
W--> 318 <400> SEQUENCE: 17
E--> 319 gtgaaatatt gctccgtcgt
320 (20)
```

Wrapped nucleics
See error summary sheet, item 1

same error

VERIFICATION SUMMARY DATE: 10/08/2002
PATENT APPLICATION: **US/10/026,106C** TIME: 13:59:25

Input Set : **A:\EP.txt**
Output Set: **N:\CRF4\10082002\J026106C.raw**

L:10 M:270 C: Current Application Number differs, Replaced Current Application Number
L:20 M:283 W: Missing Blank Line separator, <220> field identifier
L:21 M:283 W: Missing Blank Line separator, <400> field identifier
L:28 M:283 W: Missing Blank Line separator, <220> field identifier
L:29 M:283 W: Missing Blank Line separator, <400> field identifier
L:36 M:283 W: Missing Blank Line separator, <220> field identifier
L:37 M:283 W: Missing Blank Line separator, <400> field identifier
L:44 M:283 W: Missing Blank Line separator, <220> field identifier
L:45 M:283 W: Missing Blank Line separator, <400> field identifier
L:54 M:283 W: Missing Blank Line separator, <220> field identifier
L:55 M:283 W: Missing Blank Line separator, <400> field identifier
L:62 M:283 W: Missing Blank Line separator, <220> field identifier
L:63 M:283 W: Missing Blank Line separator, <400> field identifier
L:70 M:283 W: Missing Blank Line separator, <220> field identifier
L:71 M:283 W: Missing Blank Line separator, <400> field identifier
L:108 M:283 W: Missing Blank Line separator, <220> field identifier
L:109 M:283 W: Missing Blank Line separator, <400> field identifier
L:121 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:8
M:332 Repeated in SeqNo=8
L:179 M:252 E: No. of Seq. differs, <211> LENGTH:Input:522 Found:512 SEQ:8
L:185 M:283 W: Missing Blank Line separator, <220> field identifier
L:186 M:283 W: Missing Blank Line separator, <400> field identifier
L:224 M:283 W: Missing Blank Line separator, <220> field identifier
L:225 M:283 W: Missing Blank Line separator, <400> field identifier
L:238 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:10
M:332 Repeated in SeqNo=10
L:265 M:283 W: Missing Blank Line separator, <220> field identifier
L:266 M:283 W: Missing Blank Line separator, <400> field identifier
L:273 M:283 W: Missing Blank Line separator, <220> field identifier
L:274 M:283 W: Missing Blank Line separator, <400> field identifier
L:281 M:283 W: Missing Blank Line separator, <220> field identifier
L:282 M:283 W: Missing Blank Line separator, <400> field identifier
L:289 M:283 W: Missing Blank Line separator, <220> field identifier
L:290 M:283 W: Missing Blank Line separator, <400> field identifier
L:298 M:283 W: Missing Blank Line separator, <220> field identifier
L:299 M:283 W: Missing Blank Line separator, <400> field identifier
L:300 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:27 SEQ:15
L:309 M:283 W: Missing Blank Line separator, <220> field identifier
L:310 M:283 W: Missing Blank Line separator, <400> field identifier
L:317 M:283 W: Missing Blank Line separator, <220> field identifier
L:318 M:283 W: Missing Blank Line separator, <400> field identifier
L:319 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:20 SEQ:17
L:326 M:283 W: Missing Blank Line separator, <220> field identifier
L:327 M:283 W: Missing Blank Line separator, <400> field identifier
L:334 M:283 W: Missing Blank Line separator, <220> field identifier
L:335 M:283 W: Missing Blank Line separator, <400> field identifier
L:344 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:5
L:346 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19

VERIFICATION SUMMARY DATE: 10/08/2002
PATENT APPLICATION: **US/10/026,106C** TIME: 13:59:25

Input Set : **A:\EP.txt**
Output Set: **N:\CRF4\10082002\J026106C.raw**

L:346 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:5